



1/16

Input file 57h8Bcons; Output File 57h8Btra
Sequence length 3076

CCACGCGTCCGCCCACGCGTCCGGGAAGAAGCAGCTACCTCGGAGGCAGGGCGCGCAGGCGGGCGGCGATGAGAGGGGG
CGCAGCCGCAGCCCCGCGTGGGGAGCCCACCGCTAACCCCTGCACCCACCCACCCCTGCACAAAAGAGCTGGCGGGCG
CTGGCCACGTCGCCCTGGGTGACCTTCCTCGGATGCAGAATCCGCCCTGCGAGCATCCTCTTCTCTCTAGGCTCTGAA
GGCCCCGGGAGCGTGAGCGATGCCAGCTGCACCCGGGCAGGGCTCGCCTTTGTTTGCCAGTAAGGAGGAGAGGCTGTC

M G T T E A
TCAGCTGCAGAGGGGTATCCCTGCTTCAAGCCAGTGCCTCTTCCCAGCTCCC ATG GGG ACC ACC GAA GCC
T L R M E N V D V K E E W Q D E D L P R
ACG CTC CGG ATG GAA AAC GTG GAC GTG AAG GAG GAA TGG CAG GAC GAA GAT CTT CCC AGG
P L P E E T G V E L L G S P V E D T S S
CCA CTC CCA GAA GAG ACG GGG GTG GAA CTG CTT GGC AGC CCG GTG GAA GAC ACA TCC TCT
P P N T L N F N G A H R K R K T L V A P
CCT CCC AAC ACG CTA AAT TTC AAC GGA GCG CAT CGT AAG AGG AAG ACG CTG GTG GCC CCA
E I N I S L D Q S E G S L L S D D F L D
GAG ATC AAC ATT TCT CTG GAT CAG AGT GAG GGG TCC CTG CTG TCC GAT GAC TTC TTG GAT
T P D D L D I N V D D I E T P D E T D S
ACC CCT GAT GAC CTG GAT ATT AAC GTG GAT GAC ATC GAG ACC CCC GAT GAG ACC GAC TCG
L E F L G N G N E L E W E D D T P V A T
CTG GAG TTC CTG GGG AAT GGC AAC GAA CTG GAG TGG GAA GAC GAC ACC CCC GTG GCC ACC
A K N M P G D S A D L F G D G T T E D G
GCC AAG AAC ATG CCC GGG GAC AGC GCG GAT CTA TTT GGG GAC GGC ACG ACG GAG GAC GGC
S A A N G R L W R T V I I G E Q E H R I
AGC GCC GCC AAC GGG CGC CTG TGG CGG ACA GTG ATC ATC GGG GAG CAA GAG CAC CGT ATA
D L H M I R P Y M K V V T H G G Y Y G E
GAC CTG CAC ATG ATC CGG CCT TAC ATG AAA GTG GTC ACC CAC GGA GGG TAC TAC GGC GAA
G L N A I I V F A A C F L P D S S L P D
GGC CTC AAC GCC ATC ATC GTC TTC GCA GCC TGC TTC CTT CCA GAC AGC AGC CTC CCC GAC
Y H Y I M E N L F L Y V I S S L E L L V
TAC CAC TAC ATC ATG GAG AAC CTC TTC CTG TAC GTC ATC AGC AGC TTA GAG CTC CTG GTG
A E D Y M I V Y L N G A T P R R R M P G
GCT GAG GAC TAC ATG ATC GTG TAC CTG AAC GGT GCC ACG CCC CGG CGG AGG ATG CCT GGA
I G W L K K C Y Q M I D R R L R K N L K
ATC GGC TGG CTG AAG AAG TGC TAC CAG ATG ATC GAC CGG AGG TTG CGG AAA AAC CTG AAG
S L I I V H P S W F I R T V L A I S R P
TCC TTG ATC ATC GTC CAC CCC TCG TGG TTC ATT CGG ACT GTG CTG GCC ATC TCT CGC CCT
F I S V K F I N K I Q Y V H S L E D L E
TTC ATC AGC GTC AAG TTC ATC AAC AAG ATC CAG TAC GTG CAC AGC TTG GAA GAC CTG GAG

Fig. 1A



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Q L I P M E H V Q I P D C V L Q Y E E E
CAA CTC ATC CCT ATG GAA CAC GTC CAG ATC CCA GAC TGC GTC CTG CAA TAC GAA GAG GAA
R L K A R R E S A R P Q P E F V L P R S
AGA CTG AAG GCC AGG AGG GAG AGC GCG AGG CCC CAG CCG GAG TTT GTG CTG CCC AGG TCT
E E K P E V A P V E N R S A L V S E D Q 1
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E T S M S *
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CAGGTTGGAGCCACAGACACCCACCGCCACCCCGGCTGGGTCTGCGTCCCTTTCCTGTGCCTTTCCTCCAGAATGCGGC
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GCCCCTTTAACTCAGATGTCAAGCCACCGGGCAAACCCCGTCAATACCTCCCAAGGAATGAGATATGTGGACCTCA
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AGGCGGATCACCTGAGGTGAGGAGTTTGAGAACAGCCTGGCCAACATGGTGAAACCTCATCTCTACTAAAAATACAAAA
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GTGCATGCCTG

Fig. 1B

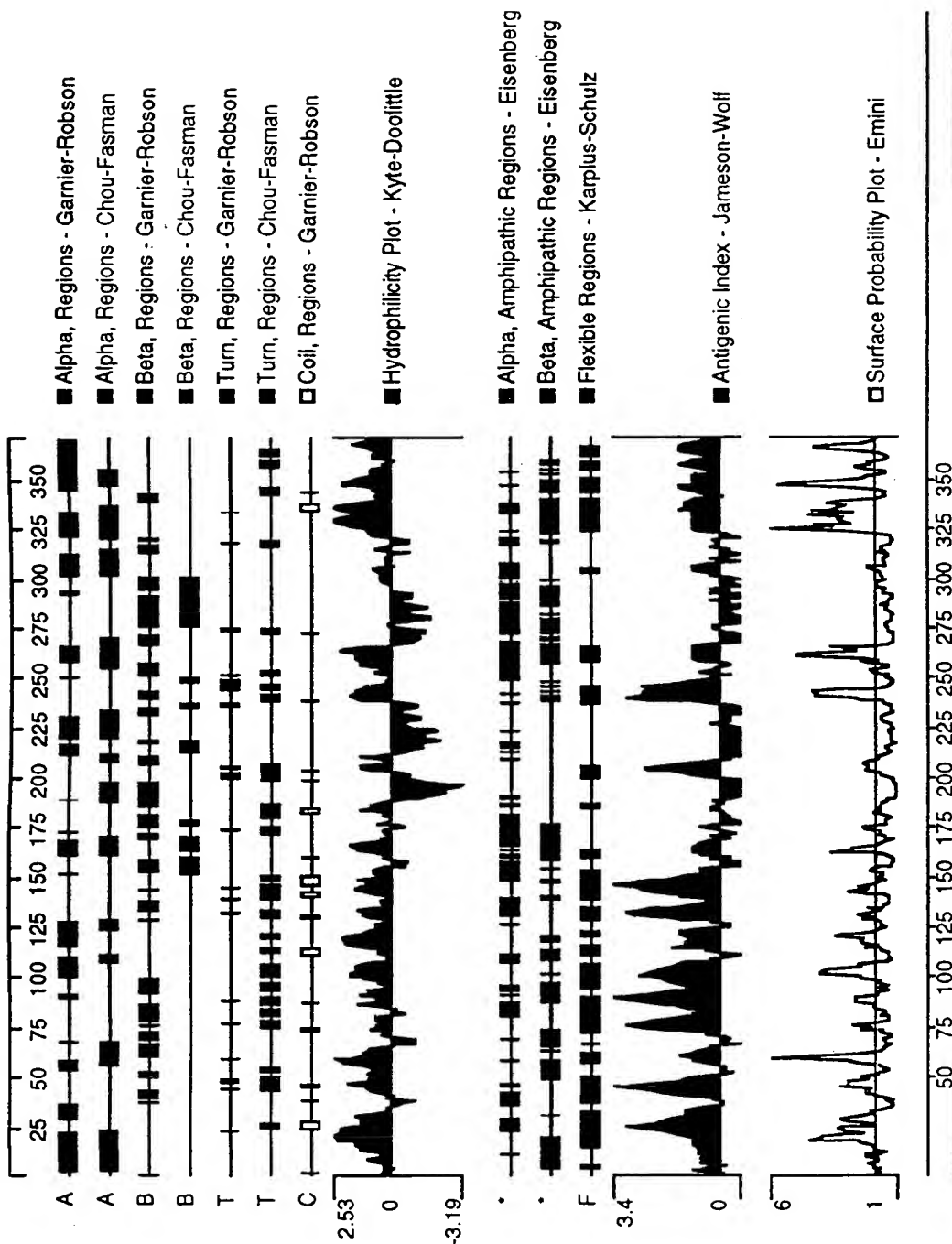


Fig. 2



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Input file Athda22f7.seq; Output File Athda22f7.tra
Sequence length 4235

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S R P N G L L S E D V G M D I P F E E G
TCA AGA CCA AAT GGA CTA CTG TCA GAG GAT GTA GGA ATG GAC ATC CCC TTT GAA GAG GGC
V L S P S A A D M R P E P P N S L D L N
GTG CTG AGT CCC AGT GCT GCA GAC ATG AGG CCT GAA CCT CCT AAT TCT CTG GAT CTT AAT 1
D T H P R R I K L T A P N I N L S L D Q
GAC ACT CAT CCT CGG AGA ATC AAG CTC ACA GCC CCA AAT ATC AAT CTT TCT CTG GAC CAA
S E G S I L S D D N L D S P D E I D I N
AGT GAA GGA TCT ATT CTC TCT GAT GAT AAC TTG GAC AGT CCA GAT GAA ATT GAC ATC AAT
V D E L D T P D E A D S F E Y T G H D P
GTG GAT GAA CTT GAT ACC CCC GAT GAA GCA GAT TCT TTT GAG TAC ACT GGC CAT GAT CCC
T A N K D S G Q E S E S I P E Y T A E E
ACA GCC AAC AAA GAT TCT GGC CAA GAG TCA GAG TCT ATT CCA GAA TAT ACG GCC GAA GAG
E R E D N R L W M T V V I G E Q E Q R I
GAA CGG GAG GAC AAC CGG CTT TGG ATG ACA GTG GTC ATT GGA GAA CAA GAG CAG CGC ATT
D M K V I E P Y R R V I S H G G D S G Y
GAC ATG AAG GTC ATC GAG CCC TAC AGG AGA GTC ATT TCT CAC GGA GGA GAT TCA GGA TAC
Y G D G L N A I I V F A A C F L P D S S
TAT GGG GAC GGT CTA AAT GCC ATC ATT GTG TTT GCC GCC TGT TTT CTG CCA GAC AGC AGT
R A D Y H Y V M E N L F L Y V I S T L E
CGG GCG GAT TAC CAC TAT GTC ATG GAA AAT CTT TTC CTA TAT GTA ATA AGT ACT TTA GAG
L M V A E D Y M I V Y L N G A T P R R R
TTG ATG GTA GCT GAA GAC TAT ATG ATT GTG TAC TTG AAT GGT GCA ACC CCA AGA AGG AGG
M P G L G W M K K C Y Q M I D R R L R K
ATG CCA GGG CTA GGC TGG ATG AAG AAA TGC TAC CAG ATG ATT GAC AGA CGG TTG AGG AAG
N L K S F I I V H P S W F I R T I L A V
AAT TTG AAA TCA TTC ATC ATT GTT CAT CCA TCT TGG TTC ATC AGA ACA ATC CTT GCT GTG
T R P F I S S K F S S K I K Y V N S L S
ACA CGA CCT TTT ATA AGT TCA AAA TTC AGC AGT AAA ATT AAA TAT GTC AAT AGC TTA TCA
882
E L S G L I P M D C I H I P E S I I N I
GAA CTC AGT GGG CTG ATC CCA ATG GAT TGC ATC CAC ATT CCA GAG AGC ATC ATC AAT ATT
D L K L K E K P *
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Fig. 3A



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AAGATATTTTATGAAATTGTGTGTA CTTTCTATTTTGCCAATTATGTGCCTCAAAGATTTTAGTTGAGCCTTAGCAAG
AAAGTAGGACCTTCCATTTCAATACTTCATTAACACGGTGTAGTGATACTTTGTCCCTTAGACTGGTGTTTACCAGTAA
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AGGACAGCCACAAACCACACAAGGTGTAAAACCATCATCAGCTAAGTGCCCGTTTTGTTCTTGTTTACCAGAATCTCCT
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GCTTTAAAACACCGTAATCTGATCATAGGCTTAAAATTAATATGAGTATTACTTTTCATGTACAAAATATTTCTTTTAT
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Fig. 3B



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TAATTTAATTGCATGTGCTAGGGAAAAGCTACCATGTACATTCACCCCAAGTAAATAGAATCCTAGATGAATCCTAGAA
AAATAATCCCTAAGCAGATAGGTAGACAGAGGTAAACATTCACATGATTTAGCTCTCTAGCTCTTGCACTCTGAACATT
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Fig. 3C

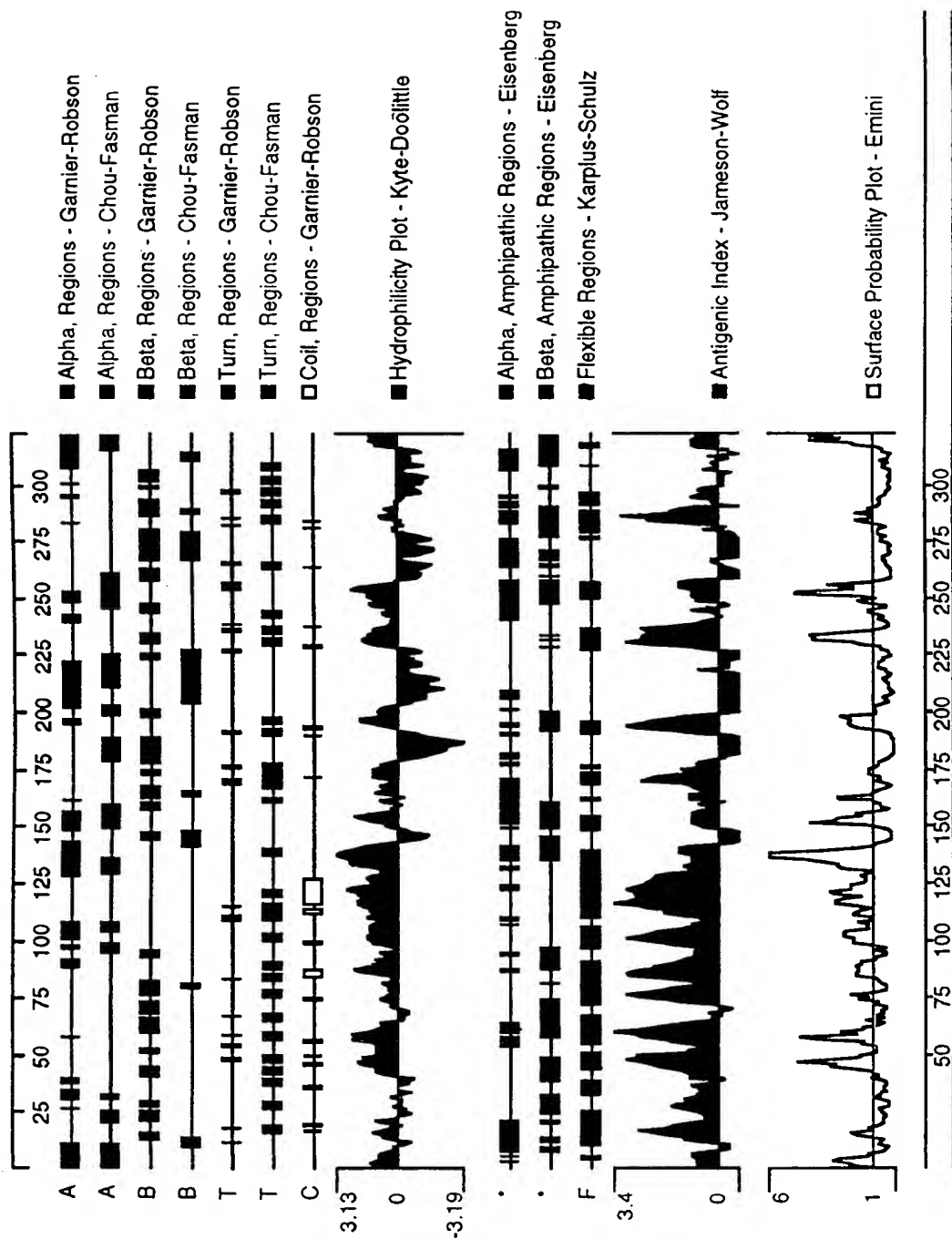


Fig. 4

Fig. 5A



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CCAGAGAGTCTTCAGCAGCTCCTCTATCCATCCCAGTTGCCCCCTACCAGCTCCTGCTCCTTTCCCTGCTAATATATTG
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GAGCTTTGTACACCACATCTGAACCTTTTATTTTAAACATAGTAAACTGTGAGCAAAGCAGTGGTGGCTGGGCAA
GCTGGTAATTAACACTGCCACTTGCTGACATGGCTCTTTTAATGTAGTTAACATAGCTGTGTGAAAGAACCAGTTTAA
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GC

Fig. 5B

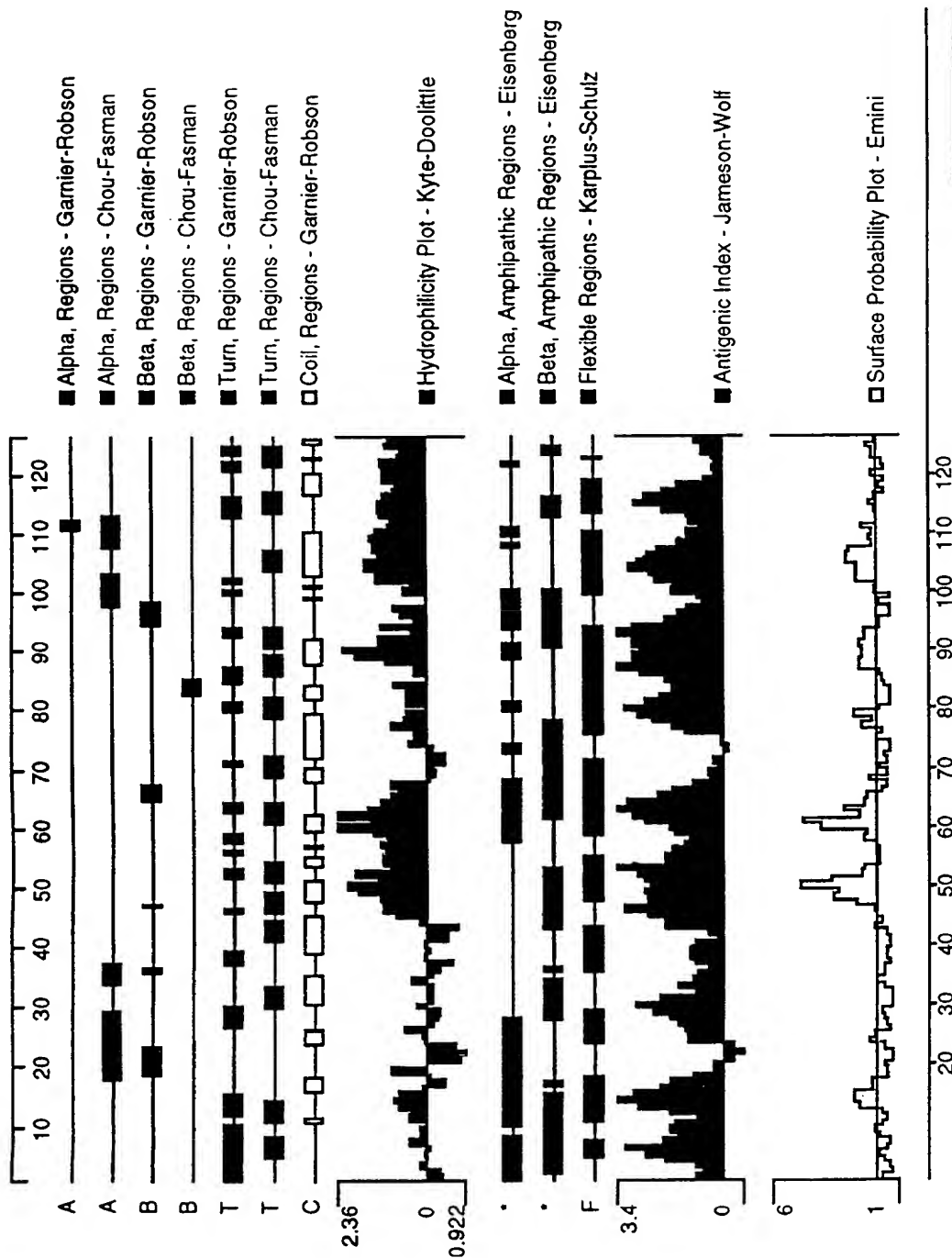


Fig. 6



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>PF00335|transmembrane4 4 transmembrane segments integral membrane proteins

Score: 1.28	Seq: 253 293	Model: 192 232
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	C++ I+ L++N+ + +++ + +L ++ + +++I	
human	253	CYQMIDRRRLRKNLKSLLIVHPSWFIRTVLAI SRPFISVKFI 293

Fig. 7



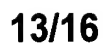
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>MILPAT00063|calret_c calreticulin calcium-binding domain

```
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REF  xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
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    +T++ R      + I ++ +S  ++++D+ L+ PD  EI D +
human  55  DTHPRRIKL-TAPNINLSLDQSEGSILSDDN-LDSPD----EI-DINVD      96
REF  xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
    KPEDWDvTkaaERqkMDDPQDEEQRWKPEDWDEDKPEHIPDEDAKEPEDW
    + D  E      E  DP++  + E +  PE  ++E+  W
human  97  ELDTPEADSFYET-GHDPTA-NKDSGQSE--SIPEYTAEEREDNRLW      142

REF  xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
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    + +E      +++  + MK
human  143  MTVVIGE-----QEQRID-MKVIE      160
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Fig. 8



Score: 0.66 Seq: 59 96 Model: 1 44

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REF  XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
*YTLIYRPDNTFEV1IDNWQVWSMSLETIWMFLP.PDNPSREIEd*
```

human

Fig. 9



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GAP of:nip2a.pep check: 3241 from:1 to:314
NIP2A | U15173 Homo sapiens BCL2/adenovirus E1B 19kD-
interacting protein 2 (BNIP2)
to: nip2b.pep check: 7307 from: 1 to: 371
NIP2B
Symbol comparison table: /usr/local/gcg_9.1/gcgcore/data/rundata/
blosum62.cmp

CompCheck: 6430

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	842	Length:	371
Ratio:	2.682	Gaps:	5
Percent Similarity:	<u>67.197</u>	Percent Identity:	<u>56.051</u>

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

nip2a.pep x nip2b.pep

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1 .....MEGVELKEEWQDEDFPIPLPEDDSIEADILAITGPEDQPGS 41
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1 MGTTEATLRMENVDVKEEWQDEDLRPLPEETGVELLGSPVEDTSSPPNT 50
42 LEVNG.NKVRKKLMAPDISLTLDPSDGSVLSDD.LDESGEIDL..DGLDT 87
      | || |: || |:|:|:..|| |:|:|||| || |:|: | :|
51 LNFNGAHRKRKTLVAPEINISLDQSEGSLLSDDFLDTPDDLINVDIET 100
88 PSE.....NSNEFEWEDDLPKPKTTEVIRKGSITEYTAAEE...KED 126
      | | | ||||| | . . . |
101 PDETDSLEFLGNGNELEWEDDTPVATAKNMPGDSADLFGDGTTEDGSAAN 150
127 GRRWRMFRIQEQRHVDMAIEPYKKVISHGGYYGDGLNAIVVFAVCFMP 176
      || || | ||:|:|: | || ||:>|||||:||||:| || |:|
151 GRLWRTVIIGQEHRIDLHMIRPYMKVVTHGGYYGEGLNAIIVFAACFLP 200
177 ESSQPNYRYLMDNLFKYVIGTLELLVAENYMIIVYLNGATTRRKMPSLGWL 226
      :|| |:| |:|:| || | . ||||| . ||||| || |:| :||
201 DSSLPDYHYIMENLFLYVISSLELLVAEDYMIIVYLNGATPRRRMPGIGWL 250
227 RKCYQQIDRRLRKNLKSIIIVHPSWFIRTLLAVTRPFISSKFSQKIRYVF 276
      :||| ||||| ||||| ||||| . ||: . |||| || ||:|
251 KKCYQMIDRRLRKNLKSIIIVHPSWFIRTVLAISRPFISVKFINKIQYVH 300
277 NLAELAELVPMEYVGIPECIKQVDQELNGKQDEPKNEQ..... 314
      .| :| |:|:|:| ||:|: | :| . | |
301 SLEDLEQLIPMEHVQIPDCVLQYEEERLKARRESARPQPEFVLPRSEKP 350
```

Fig. 10



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GAP of: nip2b.pep check:7307 from: 1 to: 371

NIP2B

to: nip2c.pep check: 3344 from: 1 to: 322

IP2C Athda22f7

Symbol comparison table:/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp

CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 871 Length: 375
Ratio: 2.705 Gaps: 4
Percent Similarity: 69.182 Percent Identity: 58.805

Match display thresholds for the alignment(s):

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: = 2
. = 1

nip2b.pep x nip2c.pep

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   || : || : || : || : ||
1 MEEETEFLELGTRISRPNGLLSEDVGMDIPFEEGV.LSPSAADMRPEPPN 49

50 TLNFNGAHRKRKTLVAPEINISLDQSEGSLLSDDFLDTPDDLDINVDDIE 99
   .|. | | :| | || ||:|||||||:|||| ||.||::|||||:::
50 SLDLNDTHPRRIKLTAPNINLSLDQSEGSILSDDNLDSPDEIDINVDELD 99

100 TPDETDSLEFLGNGNELEWEDDTPVATAKNMPGDSADLFGDGTTEGSA 149
   |||| || |:|. || | :. : | | :
100 TPDEADSFEYTGHD.....PTANKDSGQESSEIPEYTAEEERED 138

150 NGRLWRTVIIGEQRHRLHMRPYMKVVTHG...GYGEGLNAIIVFAA 196
   | ||| ||:|||| |||: .| || |:|. || |||:|||||||
139 N.RLWMTVVIGEQRIDMKVIEPYRRVISHGGDSGYGDLNAIIVFAA 187

197 CFLPDSSLPDYHYIMENLFLYVISSLELLVAEDYMIVYLNATPRRRMPG 246
   ||||| |||:||||||| |||:||||||| |||||
188 CFLPDSSRADYHYVMENLFLYVISTLELMVAEDYMIVYLNATPRRRMPG 237

247 IGWLKKCYQMIDRRRLRKNLKSIIIVHPSWFIRTVLAISRPFISVKFINKI 296
   :||:||||||| ||||| |||: ||: |||| | | .|
238 LGWMKKCYQMIDRRRLRKNLKSFIIVHPSWFIRTVLAISRPFISVKFINKI 287

297 QYVHSLEDLEQLIPMEHVQIPDCVLQYEEERLKARRESARQPPEFVLPRS 346
   .||. || :| |||: : ||: : : .
288 KYVNSLSELSGLIPMDCIHIPESIINIDLKLKEKP..... 322
```

Fig. 11



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GAP of: nip2c.pep check: 3344 from: 1 to: 322

NIP2C Athda22f7

to: nip2a.pep check: 3241 from: 1 to: 314

NIP2A | U15173 Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 2 (BNIP2)

Symbol comparison table:/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 806 Length: 331
Ratio: 2.567 Gaps: 6
Percent Similarity: 67.541 Percent Identity: 57.705

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

nip2c.pep x nip2a.pep

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1 MEEETEFLELGTRISRPNGLLSEDVGMDIPFEEGVLSPPSAADMRPE.PPN 49
      :          || .:|::: . | || |
1 .....MEGVELKEEWQDEDFPIPLPEDDSIEADILAITGPEDQPG 40

50 SLDLNDTHPRRIKLTAPNINLSLDQSEGSILSDDNLDSPDEIDINVDEL 99
   ||:.| | : || ||.|.|.|| |:||:|||| || |||: | ||
41 SLEVNGNKVRK.KLMAPDISLTLDPSDGSVLSDD.LDESGEIDL..DGLD 86

100 TPDE.ADSFEYTGHDPTANKDSGQESSEIPEYTAEEEREDNRLWMTVVIG 148
    || | .. ||: | | |||| ||:|| | | ||
87 TPSENSNEFEWEDDLPKPKTTEVIRKGSITEYTAEEKEDGRRWRMFRIG 136

149 EQEQRIDMKVIEPYRRVISHGGDSGYGDGLNAIIVFAACFLPDSSRADY 198
   ||: |:||| ||||:||||| | ||||| |||||;||| ||:|:|. .|
137 EQDHRVDMKAIEPYKKVISHG...GYGDGLNAIVVFAVCFMPRESSQPNY 183

199 HYVMENLFLYVISTLELMVAEDYMIVYLNAGATPRRRMPGLGWMKKCYQMI 248
   |.:||| ||| ||||:||||.||||||| ||:|| |||:|||| |
184 RYLMDNLFKYVIGTLELLVAENYMIVYLNAGATRRKMPSLGWLRCYQYQI 233

249 DRRLRKNLKSFIIVHPSWFIRTILAVTRPFISSKFSSKIYVNSLSELSG 298
   ||||| ||||| |||||:||||| ||||| ||:|| .|.||.
234 DRRLRKNLKSIIIVHPSWFIRTLLAVTRPFISSKFSQKIRYVFNLAELAE 283

299 LIPMDCIHIPESIINIDLKLEKP..... 322
   |:||: |:| | :|. | |
284 LVPMEYVGIIPECIKQVDQELNGKQDEPKNEQ 314
```

Fig. 12